Figure 1

Figure 2

Figure 3

Figure 4

Figure 5

DNA Sequence of ARBP cDNA (SEQ ID No. 3) and predicted amino acid
sequence of encoded protein (SEQ ID No. 4)

```
                       GCTGGCCGGGTCGACCCTGGTGTCATCCGTTTAGGAAGCGGCTTCACCGCCAACAGCACGGCC
1   Met Ala Gly Ala Leu Val Arg Lys Ala Ala Asp Tyr Val Arg Ser Lys Asp Phe Arg Asp
    ATG GCT GGA GCT CTG GTG CGC AAA GCA GCG GAC TAT GTC CGG AGC AAG GAC TTC CGG GAC
21  Tyr Leu Met Ser Thr His Phe Trp Gly Pro Val Ala Asn Trp Gly Leu Pro Ile Ala Ala
    TAT CTC ATG AGT ACG CAC TTC TGG GGC CCA GTT GCC AAC TGG GGT CTC CCC ATT GCT GCT
41  Ile Asn Asp Met Lys Lys Ser Pro Glu Ile Ile Ser Gly Arg Met Thr Phe Ala Leu Cys

    ATC AAT GAC ATG AAG AAA TCT CCA GAG ATT ATC AGT GGG CGG ATG ACT TTC GCC CTC TGT
61  Cys Tyr Ser Leu Thr Phe Met Arg Phe Ala Tyr Lys Val Gln Pro Arg Asn Trp Leu Leu
    TGC TAT TCT CTG ACA TTC ATG AGA TTT GCC TAC AAG GTA CAA CCC CGA AAC TGG CTT CTG
81  Phe Ala Cys His Val Thr Asn Glu Val Ala Gln Leu Ile Gln Gly Gly Arg Leu Ile Asn
    TTT GCG TGC CAT GTG ACA AAC GAA GTC GCT CAG CTC ATT CAG GGA GGA CGA CTT ATC AAC
101 Tyr Glu Met Ser Lys Arg Pro Ser Ala  *
    TAC GAG ATG AGT AAG CGG CCA TCT GCC TAG
CAGTGCAAGGACCAGCTCTTGAAAGGGACAGTGCT
CCAGCCACTGTTGCGGCCACAGATCACGTCAGCATGAATAGTCGTGCTGAGGGGAAAACACGGAAGACTATCTTTAATGACCATG
CCAACATTATTGAATAGCCAAGAATCCCCAAACCAACTCTCGGCTGCCTTATCAATGCTAAACTTTATTTGTCTTCATCAGGAGT
AGTTCAAAATATGCAGCTAATTTAATAATTTTGAATGATGTTATCTATAGCAATCTGTAGTAATATGTATATTATCTATTGGGAT
TTGTGTAATAAAAAATCTAAGGGAACAAAACTTTATAACTACAAGCACTTAAGTCCTCAAAATTCTTGACTTTTTCTTTAATGAC
TATAGTATAACCCTCAGTTGGTCACATGTCTACACATAATTTCCAGTGATAACAAGTAGCGGTGTTTTCCATATGTAATTCAGAT
CTGAACTTAATGGCAATAAATGGTTTAAATATTTGCGAAAAAAAAAAA
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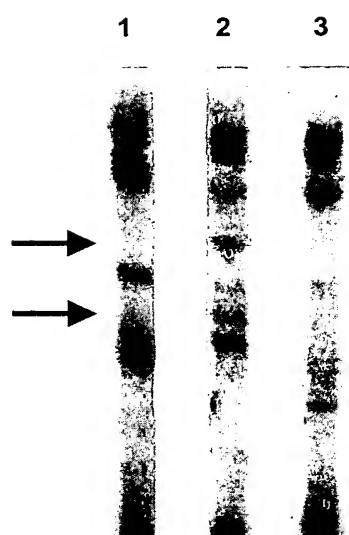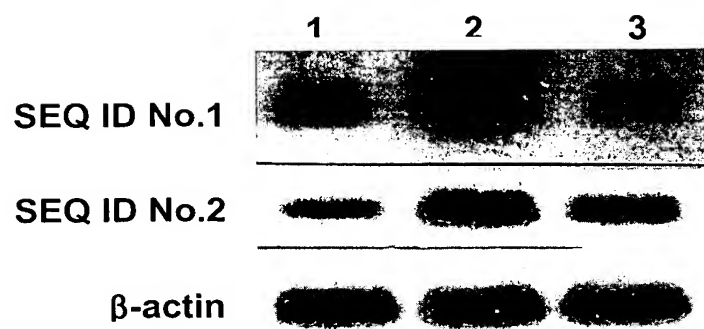
Figure 6

```
Sequence 1:  human                102 aa
Sequence 2:  rat                  109 aa
Sequence 3:  mouse                109 aa



Sequences (1:2) Aligned.  Score: 97.0588
Sequences (1:3) Aligned.  Score: 96.0784
Sequences (2:2) Aligned.  Score: 100
Sequences (2:3) Aligned.  Score: 99.0826
Sequences (3:2) Aligned.  Score: 99.0826
Sequences (3:3) Aligned.  Score: 100


rat      MAGALVRKAADYVRSKDFRDYLMSTHFWGPVANWGLPIAAINDMKKSPEIISGRMTFALC
mouse    MAGALVRKAADYVRSKDFRDYLMSTHFWGPVANWGLPIAAINDMKKSPEIISGRMTFALC
human    MAGALVRKAADYVRSKDFRDYLMSTHFWGPVANWGLPIAAINDMKKSPEIISGRMTFALC
         ***********************************************************

rat      CYSLTFMRFAYKVQPRNWLLFACHVTNEVAQLIQGGRLINYEMSKRPSA
mouse    CYSQTFMRFAYKVQPRNWLLFACHVTNEVAQLIQGGRLINYEMSKRPSA
human    CYSLTFMRFAYKVQPRNWLLFACHATNEVAQLIQGGRLIKHE-------
         *** *******************.***************::*
```

Figure 7

```
Homo sapiens NM_016098, mRNA
Length = 988

Score =  361 bits (182), Expect = 1e-96
Identities = 284/318 (89%)
Strand = Plus / Plus

Query: 56   gcacggccatggctggagctctggtgcgcaaagcagcggactatgtccggagcaaggact 115
            |||| |||||||| || ||  ||||||| |||||  |||||||||||||| |||||||| |
Sbjct: 115  gcacagccatggcgggcgcgttggtgcggaaagcggcggactatgtccgaagcaaggatt 174

Query: 116  tccgggactatctcatgagtacgcacttctggggcccagttgccaactggggtctcccca 175
            ||||||||||  |||||||||||||||||||||||||||||||  |||||||||||| ||||
Sbjct: 175  tccgggactacctcatgagtacgcacttctggggcccagtagccaactggggtcttccca 234

Query: 176  ttgctgctatcaatgacatgaagaaatctccagagattatcagtgggcggatgactttcg 235
            ||||||| |||||||| |||||  || ||||||||||||||||||||||||||||||| | |
Sbjct: 235  ttgctgccatcaatgatatgaaaaagtctccagagattatcagtgggcggatgacatttg 294

Query: 236  ccctctgttgctattctctgacattcatgagatttgcctacaaggtacaaccccgaaact 295
            |||||||||||||||| ||||||||||||||||||||||||||||||| || || ||||
Sbjct: 295  ccctctgttgctattctttgacattcatgagatttgcctacaaggtacagcctcggaact 354

Query: 296  ggcttctgtttgcgtgccatgtgacaaacgaagtcgctcagctcattcagggaggacgac 355
            |||||||||||| |||||  |  ||||| ||||| || ||||||| |||||| ||||| | |
Sbjct: 355  ggcttctgtttgcatgccacgcaacaaatgaagtagcccagctcatccagggagggcggc 414

Query: 356  ttatcaactacgagatga 373
            |||||||  |||||||||
Sbjct: 415  ttatcaaacacgagatga 432

 Score = 56.0 bits (28), Expect = 1e-04
 Identities = 31/32 (96%)
 Strand = Plus / Plus

Query: 857  aacttaatggcaataaatggtttaaatatttg 888
            ||||||||||||||||||| |||||||||||
Sbjct: 926  aacttaatggcaataaatgatttaaatatttg 957

 Score = 46.1 bits (23), Expect = 0.092
 Identities = 32/35 (91%)
 Strand = Plus / Plus

Query: 595  gagtagttcaaaatatgcagctaatttaataattt 629
            ||||||  ||||||||||||||   ||||||||||||
Sbjct: 660  gagtagctcaaaatatgcaattaatttaataattt 694

 Score = 44.1 bits (22), Expect = 0.36
 Identities = 95/118 (80%), Gaps = 1/118 (0%)
 Strand = Plus / Plus

Query: 651  atctgtagtaatatgtatattatctattgggatttgtgtaataaaaaatctaagggaaca 710
            ||||| ||||||||||||||| |||||||| | |||||   |||| ||||||   ||| |||||
Sbjct: 708  atctgcagtaatatgtatatcatctattagaatttacttaatgaaaaactgaagagaaca 767

Query: 711  aaactttataactacaagcacttaagtcctcaaaattcttgactttttctttaatgac 768
            ||| ||| |||| || |||||||||||||| |||      |||||| || || ||||||||||
Sbjct: 768  aaa-tttgtaaccactagcacttaagtactcctgattcttaacattgtctttaatgac 824
```

Figure 8

Mus musculus adult male kidney cDNA, RIKEN full-length enriched library,
clone:0610007A16 product:brain protein 44-like, full insert sequence
Length = 886
Score = 1374 bits (693), Expect = 0.0
Identities = 833/875 (95%), Gaps = 6/875 (0%)
Strand = Plus / Plus

```
Query:  19  ggtgtcatccgtttaggaagcggcttcaccgccaacagcacggccatggctggagctctg  78
            |||||||||  ||  ||||  ||||||||||||||||||||||  |||||||||||||  |||   |||
Sbjct:  13  ggtgtcatctgtctaggtagcggcttcaccgccaacggcacggccatggctggagcgctg  72

Query:  79  gtgcgcaaagcagcggactatgtccggagcaaggacttccgggactatctcatgagtacg  138
            |||||||||||  ||||||||||||||||||||||||||||||||||||||||||||||||||  |||||
Sbjct:  73  gtgcgcaaagcggcggactatgtccggagcaaggacttccgggactatctcatgagtacg  132

Query: 139  cacttctggggcccagttgccaactggggtctccccattgctgctatcaatgacatgaag  198
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 133  cacttctggggcccagttgccaactggggtctccccattgctgctatcaatgacatgaag  192

Query: 199  aaatctccagagattatcagtgggcggatgactttcgccctctgttgctattctctgaca  258
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 193  aaatctccagagattatcagtgggcggatgactttcgccctctgttgctattctctgaca  252

Query: 259  ttcatgagatttgcctacaaggtacaaccccgaaactggcttctgtttgcgtgccatgtg  318
            |||||||||||||||||||||||||||||  ||||||||  ||||||||  |||||||||
Sbjct: 253  ttcatgagatttgcctacaaggtacaacctcgaaactggcttttgtttgcatgccatgta  312

Query: 319  acaaacgaagtcgctcagctcattcaggggaggacgacttatcaactacgagatgagtaag  378
            |||||||||||  ||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 313  acaaacgaagtagctcagctcattcagggaggacgacttatcaactacgagatgagtaag  372

Query: 379  cggccatctgcctagcagtgcaaggaccagctcttgaaagggacagtgctccagccactg  438
            ||||||||||  ||||  ||  ||||||||||||||||||  |||||||||||||||||||
Sbjct: 373  cggccatctgcatagcggtacaaggaccagctcttgaaagagacagtgctccagccactg  432

Query: 439  ttgcggccacagatcacgtcagcatgaatagtcgtgctgaggggaaaacacggaagacta  498
            |||  |||||||||||||  ||||||||||  |||||||||||  |||||||||  |  |||
Sbjct: 433  ctgcagccacagatcatgtcagcatgagtagtcgtgctgaagggaaaacacagaatgcta  492

Query: 499  tctttaatgaccatgccaacattattgaatagccaagaatccccaaaccaactctcggct  558
            ||  |||||||||||||||||||||||||||||||  |||  ||||  |||||  |||||  |||
Sbjct: 493  tc-ttaatgaccatgccaacattattgaatagccgagagtccctaaacccactctctgct  551

Query: 559  gccttatcaatgctaaactttatttgtcttcatcaggagtagttcaaaatatgcagctaa  618
            |||||||||||||||||||  |||||||||||||||  ||||||||||||||||||  ||||
Sbjct: 552  gccttatcaatgctaaaccttatttgtcttcatcaagagtagttcaaaatatgcaactaa  611

Query: 619  tttaataattttgaatgatg---ttatctatagcaatctgtagtaatatgtatattatct  675
            |||||||||||||||||||||   |||||||||||||||||||||||||||||||||||||
Sbjct: 612  tttaataattttgaatgatggttttatctatagcaatctgtagtaatatgtatattatct  671

Query: 676  attgggatttgtgtaataaaaaatctaagggaacaaaactttataactacaagcacttaa  735
            ||||||||||||||||||||||||||||||||||||||  ||||||||||||||||||||
Sbjct: 672  attgggatttgtgtaataaaaaatctaagggaacaaaattttataactacaagcacttaa  731

Query: 736  gtcctcaaaattcttgactttttctttaatgactatagtataaccctcagttggtcacat  795
            ||  |||||||||||||||||||||||||||||  ||||||  |||||||||||||||||
Sbjct: 732  gtactcaaaattcttgactttttctttaatgacaatagta-aaccctcagttggtcacat  790

Query: 796  gtctacacataatttccagtgataacaagtagcggtgtttccatatgtaattcagatct  855
            ||||||||||||||||||||||||||||||  ||||||||||||||||||  |||||||
Sbjct: 791  gtctacacataatttccagtgataacaagtatcggtgttttccatatgtaactcagatct  850

Query: 856  g-aacttaatggcaataaatggtttaaatatttgc  889
            |  |||||||||||||||||||||||||||||||||||
Sbjct: 851  gtaacttaatggcaataaatggtttaaatatttgc  885
```

Figure 9

SUBJECT IS MOUSE, QUERY IS HUMAN

```
Homo sapiens NM_016098, mRNA
Length = 988
Score =  404 bits (204), Expect = e-110
Identities = 291/320 (90%)
Strand = Plus / Plus

Query: 48   cggcacggccatggctggagcgctggtgcgcaaagcggcggactatgtccggagcaagga 107
            ||||||  |||||| ||   || ||| || ||| ||||||||||||||||||  |||||| ||
Sbjct: 113  cggcacagccatggcggggcgcgttggtgcggaaagcggcggactatgtccgaagcaagga 172

Query: 108  cttccgggactatctcatgagtacgcacttctggggcccagttgccaactggggtctccc 167
            ||||||||||||| || ||||||||||||||||||||||||||| |||||| |||||||| ||
Sbjct: 173  tttccgggactacctcatgagtacgcacttctggggcccagtagccaactggggtcttcc 232

Query: 168  cattgctgctatcaatgacatgaagaaatctccagagattatcagtgggcggatgacttt 227
            |||||||| ||||||||| |||||| ||||||||||||||||||||||||||||||||| ||
Sbjct: 233  cattgctgccatcaatgatatgaaaaagtctccagagattatcagtgggcggatgacatt 292

Query: 228  cgccctctgttgctattctctgacattcatgagatttgcctacaaggtacaacctcgaaa 287
            ||||||||||||||||||| |||||||||||||||||||||||||||||||| |||| ||
Sbjct: 293  tgccctctgttgctattctttgacattcatgagatttgcctacaaggtacagcctcggaa 352

Query: 288  ctggcttttgtttgcatgccatgtaacaaacgaagtagctcagctcattcagggaggacg 347
            |||||| |||||||||||||||| | ||||||| ||||||||| ||||||| |||||||| ||
Sbjct: 353  ctggcttctgtttgcatgccacgcaacaaatgaagtagcccagctcatccagggagggcg 412

Query: 348  acttatcaactacgagatga 367
            ||||||||  ||||||||||
Sbjct: 413  gcttatcaaacacgagatga 432


  Score =  63.9 bits (32), Expect = 4e-07
  Identities = 35/36 (97%)
  Strand = Plus / Plus

Query: 849  ctgtaacttaatggcaataaatggtttaaatatttg 884
            ||||||||||||||||||||||||| ||||||||||
Sbjct: 922  ctgtaacttaatggcaataaatgatttaaatatttg 957


  Score =  58.0 bits (29), Expect = 2e-05
  Identities = 35/37 (94%)
  Strand = Plus / Plus

Query: 586  aagagtagttcaaaatatgcaactaatttaataattt 622
            |||||||| |||||||||||||| |||||||||||||
Sbjct: 658  aagagtagctcaaaatatgcaattaatttaataattt 694


  Score =  52.0 bits (26), Expect = 0.001
  Identities = 96/118 (81%), Gaps = 1/118 (0%)
  Strand = Plus / Plus

Query: 647  atctgtagtaatatgtatattatctattgggatttgtgtaataaaaaatctaagggaaca 706
            ||||| |||||||||||||||| ||||||| ||||   |||| ||||| ||| |||||
Sbjct: 708  atctgcagtaatatgtatatcatctattagaatttacttaatgaaaaactgaagagaaca 767

Query: 707  aaattttataactacaagcacttaagtactcaaaattcttgacttttttctttaatgac 764
            |||  ||| ||||| || |||||||||||||  ||||||| || || ||||||||||
Sbjct: 768  aaa-tttgtaaccactagcacttaagtactcctgattcttaacattgtctttaatgac 824


  Score =  46.1 bits (23), Expect = 0.091
  Identities = 35/39 (89%)
  Strand = Plus / Plus

Query: 519  aatagccgagagtccctaaacccactctctgctgcctta 557
            ||||| ||||||| ||  |||||  ||||||||||||||||
Sbjct: 589  aatagctgagagtttctaaaccaactctctgctgcctta 627
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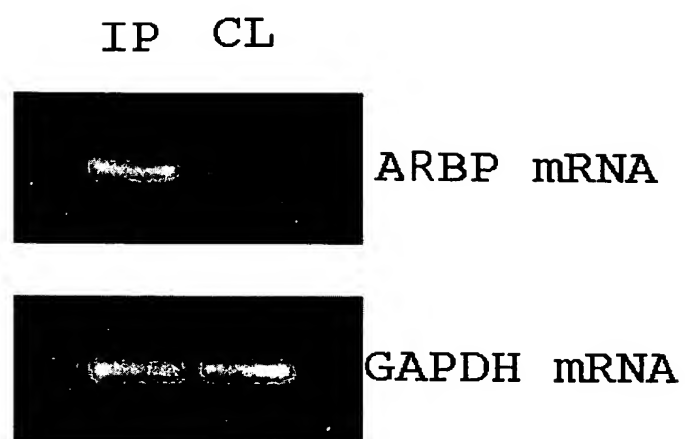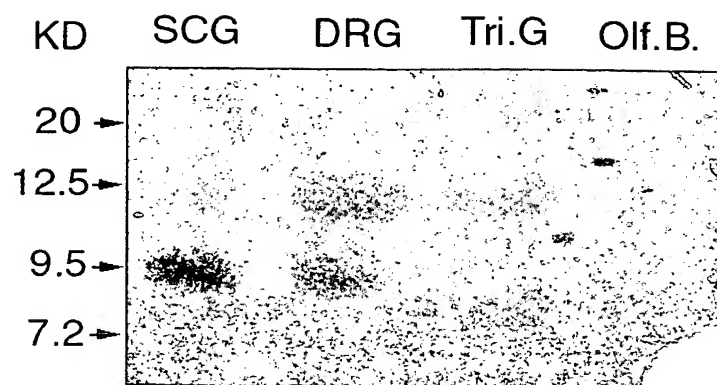
Figure 10

IP   CL

ARBP mRNA

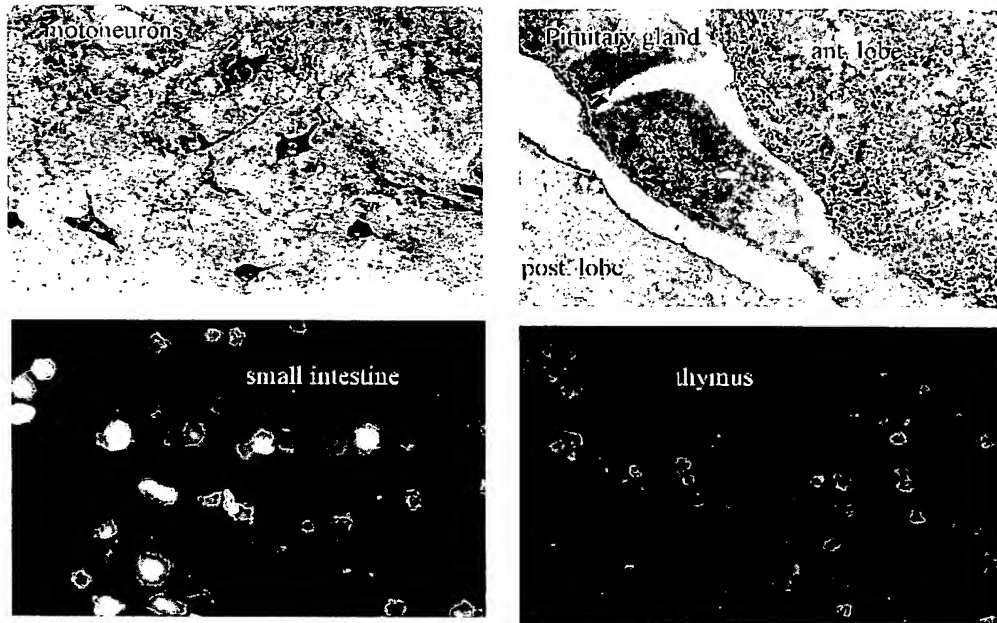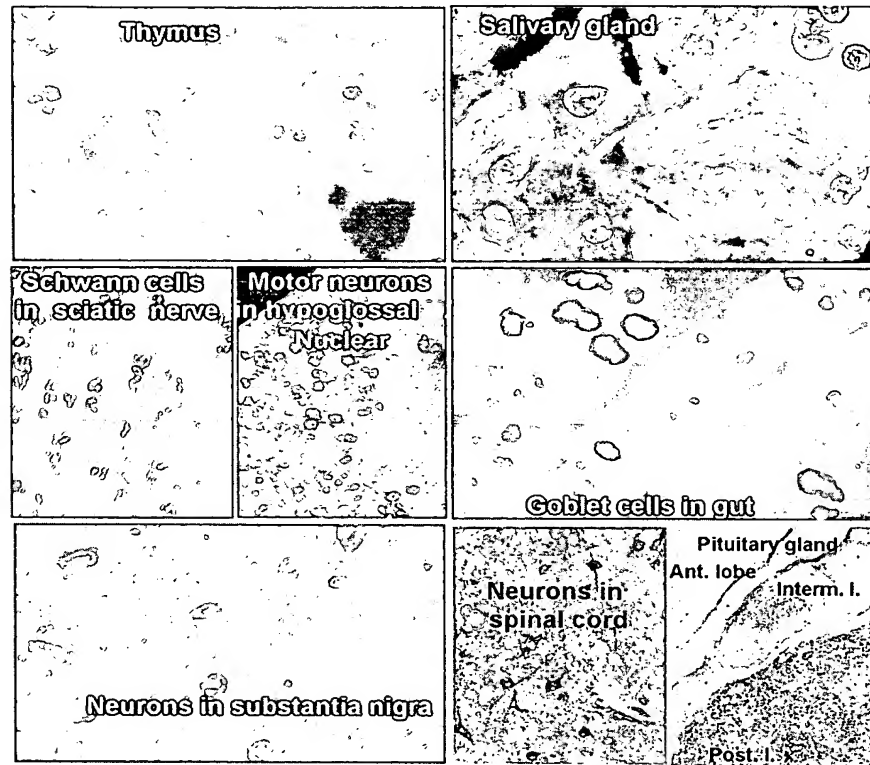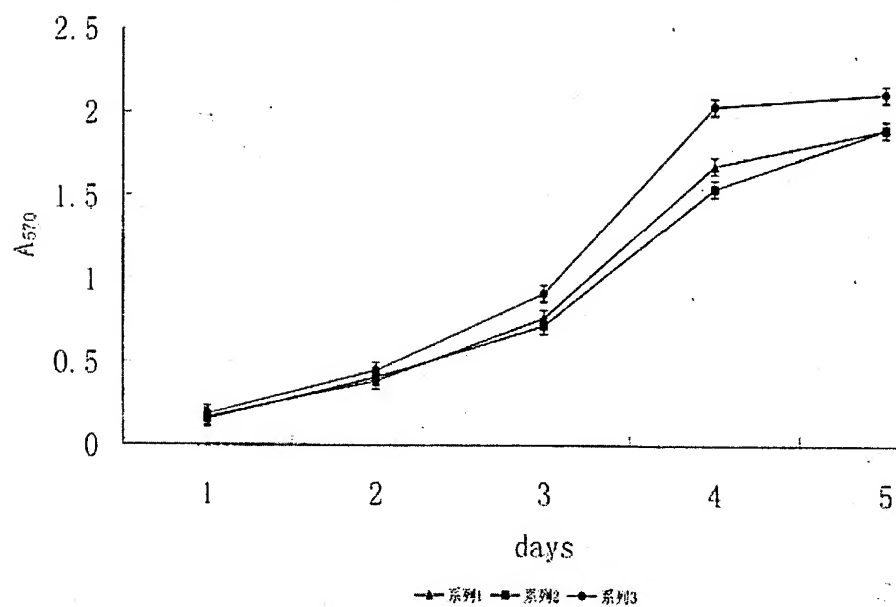GAPDH mRNA

Figure 11

Figure 12

Figure 13

Figure 14

1, R2L1/R2L1-pcD 2, R2L1-ARBPF 3, R2L1-ARBPR

Figure 15

12h

24h

48h

R2L1/R2L1-pcD   R2L1-ARBPR   R2L1-ARBPF